

SEQUENCE LISTING

<110> Diversa Corporation
Hitchman, Timothy
Robertson, Dan
Gray, Kevin
Hiraiwa, Masao
Phillips, Yoko

<120> LACCASES, NUCLEIC ACIDS ENCODING THEM AND METHODS FOR MAKING AND USING THEM

<130> 564462012640

<140> To Be Assigned

<141> Concurrently Herewith

<150> 60/494,472

<151> 2003-08-11

<160> 26

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1542

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 1

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aaggccaaaa	gaaatgaaaa	cgtttatgtg	aaatggatga	ataaccttcc	ttcagagcat	240
tttcttccga	ttgatcacac	cattcatcac	agtgcagcc	agcatgccga	acccgaggtg	300
aaaaccgtcg	ttcatttaca	cggcggcgtc	actccagatg	acagcgacgg	ttatcctgag	360
gcctggtttt	ctaaagactt	tgaacaaaaca	ggcccttatt	ttaaacgaga	ggtttaccat	420
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gtacggcacg	aaagaatata	aaacctccga	acattgaagc	tggcaggaac	tcaagatcaa	1140
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tttgaagagc	gcggagaact	ggcctacacc	ggacccgcgg	ttccgcccgc	accaagtga	1380
aaaggctgga	aagacacggg	tcagtcccac	gccggtgaag	tcctgagaat	cgccgtaaca	1440
ttcgggcat	acactgggcg	gtacgtatgg	cattgccaca	ttcttgagca	tgaagactat	1500

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1542

<210> 2

<211> 514

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 2

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			20					25					30		
Glu	Glu	Cys	Tyr	His	Gln	Leu	His	Arg	Asp	Leu	Pro	Pro	Thr	Arg	Leu
		35					40					45			
Trp	Gly	Tyr	Asn	Gly	Leu	Phe	Pro	Gly	Pro	Thr	Ile	Lys	Ala	Lys	Arg
	50					55					60				
Asn	Glu	Asn	Val	Tyr	Val	Lys	Trp	Met	Asn	Asn	Leu	Pro	Ser	Glu	His
					70					75					80
Phe	Leu	Pro	Ile	Asp	His	Thr	Ile	His	His	Ser	Asp	Ser	Gln	His	Ala
				85					90					95	
Glu	Pro	Glu	Val	Lys	Thr	Val	Val	His	Leu	His	Gly	Gly	Val	Thr	Pro
			100					105					110		
Asp	Asp	Ser	Asp	Gly	Tyr	Pro	Glu	Ala	Trp	Phe	Ser	Lys	Asp	Phe	Glu
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Gln	Thr	Gly	Pro	Tyr	Phe	Lys	Arg	Glu	Val	Tyr	His	Tyr	Pro	Asn	Gln
	130					135					140				
Gln	Arg	Gly	Ala	Ile	Leu	Trp	Tyr	His	Asp	His	Ala	Met	Ala	Leu	Thr
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Arg	Leu	Asn	Val	Tyr	Ala	Gly	Leu	Ile	Gly	Ala	Tyr	Ile	Ile	His	Glu
				165					170					175	
Pro	Lys	Glu	Lys	Arg	Leu	Lys	Leu	Pro	Ser	Gly	Glu	Tyr	Asp	Val	Pro
			180					185					190		
Leu	Leu	Ile	Thr	Asp	Arg	Thr	Ile	Asn	Glu	Asp	Gly	Ser	Leu	Phe	Tyr
		195					200					205			
Pro	Ser	Gly	Pro	Glu	Asn	Pro	Ser	Pro	Ser	Leu	Pro	Asn	Pro	Ser	Ile
		210				215					220				
Val	Pro	Ala	Phe	Cys	Gly	Asp	Thr	Ile	Leu	Val	Asn	Gly	Lys	Ala	Trp
					230				235						240
Pro	Tyr	Met	Glu	Val	Glu	Pro	Arg	Lys	Tyr	Arg	Phe	Arg	Val	Ile	Asn
				245					250					255	
Ala	Ser	Asn	Thr	Arg	Thr	Tyr	Asn	Leu	Ser	Leu	Asp	Asn	Gly	Gly	Glu
			260					265					270		
Phe	Ile	Gln	Ile	Gly	Ser	Asp	Gly	Gly	Leu	Leu	Pro	Arg	Ser	Val	Lys
		275					280					285			
Leu	Asn	Ser	Phe	Ser	Ile	Ala	Pro	Ala	Glu	Arg	Phe	Asp	Ile	Leu	Ile
		290				295					300				
Asp	Phe	Ala	Ala	Phe	Glu	Gly	Gln	Ser	Ile	Ile	Leu	Ala	Asn	Ser	Glu
					310					315					320
Gly	Cys	Gly	Gly	Asp	Val	Asn	Pro	Glu	Thr	Asp	Ala	Asn	Ile	Met	Gln
				325					330					335	
Phe	Arg	Val	Thr	Lys	Pro	Leu	Ala	Gln	Lys	Asp	Glu	Ser	Arg	Lys	Pro
			340					345					350		
Lys	Tyr	Leu	Ala	Ser	Tyr	Pro	Ser	Val	Arg	His	Glu	Arg	Ile	Gln	Asn
		355					360					365			
Leu	Arg	Thr	Leu	Lys	Leu	Ala	Gly	Thr	Gln	Asp	Gln	Tyr	Gly	Arg	Pro
						375									380

Val Leu Leu Leu Asn Asn Lys Arg Trp His Asp Pro Val Thr Glu Ala
 385 390 395 400
 Pro Lys Ala Gly Ser Thr Glu Ile Trp Ser Ile Ile Asn Pro Thr Arg
 405 410 415
 Gly Thr His Pro Ile His Leu His Leu Val Ser Phe Arg Val Leu Asp
 420 425 430
 Arg Arg Pro Phe Asp Thr Ala Arg Phe Glu Glu Arg Gly Glu Leu Ala
 435 440 445
 Tyr Thr Gly Pro Ala Val Pro Pro Pro Pro Ser Glu Lys Gly Trp Lys
 450 455 460
 Asp Thr Val Gln Ser His Ala Gly Glu Val Leu Arg Ile Ala Val Thr
 465 470 475 480
 Phe Gly Pro Tyr Thr Gly Arg Tyr Val Trp His Cys His Ile Leu Glu
 485 490 495
 His Glu Asp Tyr Asp Met Met Arg Pro Met Asp Val Ile Asp Pro His
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 Lys Ser

<210> 3

<211> 1626

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 3

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gtgtcgatcc	tgccctggacc	actcactcgc	gtctggcggt	acgacggcaa	agtcgtgaag	240
ggcgatcccg	gcaacctggc	tttcctgtcg	aacggttatt	taccggtggt	gcgcgtgcgg	300
cgcgacacaga	aagtgcgcat	cgatttcgtc	aaccagttag	ctgagccgac	catcatccac	360
tggcatggcc	tgtacgtgcc	agcagcaatg	gatggacatc	cgcgcaatgc	ggtttcgacc	420
ggcgagcact	acgtgtacga	gttcgagatc	gccaaccagg	cagggacgta	ctggtttcat	480
gcgcaccccc	acggtcgtac	gggagcacia	atttacttcg	gactggcggg	ggtattgatc	540
gtcgacgatg	aggaggcggc	cgccgggttg	cccgaaggtc	cgtagcatgt	accgctcgtg	600
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ctgaatgggt	cgaacacgcg	tatctacaag	cttgctgga	gcgaccggac	acccctcacg	900
gtaatcggtg	cggacggcgg	actgctggaa	cggccgggtg	cgcgccaata	cgtagcgtg	960
gcgcggcgcc	agcgcggtga	cgtctgggtg	gatttcagtc	gatggccggt	cggcacgaag	1020
ctgacgctgc	agagtctggc	gttcgacggc	gtcctggcca	tgggcggcgt	gatcggaac	1080
acctcgttac	cgagcggcgc	gtcgttccc	gtcctgaagg	tcggcgctcg	ccagcgtgcg	1140
aacacaaaga	tggaaactgcc	ggcgcggtc	gcatcgctgc	caccggtgcg	ccctcaggac	1200
gccgtcaatg	cgcacaatcc	gaaggtgttc	aacatcacga	tgggcatgat	ggtctggggc	1260
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cacgttcacg	ggctgcagtt	ccgtgtgctg	gagcgtaccg	tccagccgga	tttcagagcc	1440
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<210> 4

<211> 541

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<221> SIGNAL

<222> (1)...(37)

<400> 4

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20      25      30
Arg Glu Val Arg Ala Gln Pro Arg Ala Ala Asn Pro Gln Phe Ile Pro
35      40      45
Asp Leu Glu Ile Gln Leu Asn Ala Arg Glu Asp His Val Ser Ile Leu
50      55      60
Pro Gly Pro Leu Thr Arg Val Trp Arg Tyr Asp Gly Lys Val Val Lys
65      70      75      80
Gly Asp Pro Gly Asn Leu Ala Phe Leu Ser Asn Gly Tyr Leu Pro Val
85      90      95
Val Arg Val Arg Arg Gly Gln Lys Val Arg Ile Asp Phe Val Asn Gln
100     105     110
Leu Ala Glu Pro Thr Ile Ile His Trp His Gly Leu Tyr Val Pro Ala
115     120     125
Ala Met Asp Gly His Pro Arg Asn Ala Val Ser Thr Gly Glu His Tyr
130     135     140
Val Tyr Glu Phe Glu Ile Ala Asn Gln Ala Gly Thr Tyr Trp Phe His
145     150     155     160
Ala His Pro Asp Gly Arg Thr Gly Ala Gln Ile Tyr Phe Gly Leu Ala
165     170     175
Gly Val Leu Ile Val Asp Asp Glu Glu Ala Ala Ala Gly Leu Pro Glu
180     185     190
Gly Pro Tyr Asp Val Pro Leu Val Ile Gln Asp Arg Thr Phe Asp Asp
195     200     205
Arg Asn Gln Phe Thr Tyr Leu Ala Glu Gly Asn Glu Gly Met Met Gly
210     215     220
Gly Met Met Gly Asn Gly Gly Met Met Gly Arg Gly Gly Met Met Gly
225     230     235     240
Gly Gly Gly Met Gly Gln Met Met Ala Arg Met Met Gly Phe Leu Gly
245     250     255
Asp Arg Ile Leu Val Asn Gly Lys Pro Asp Phe Val Leu Pro Val Ala
260     265     270
Ala Arg Ala Tyr Arg Leu Arg Leu Leu Asn Gly Ser Asn Thr Arg Ile
275     280     285
Tyr Lys Leu Ala Trp Ser Asp Arg Thr Pro Leu Thr Val Ile Gly Thr
290     295     300
Asp Gly Gly Leu Leu Glu Arg Pro Val Thr Arg Gln Tyr Val Thr Leu
305     310     315     320
Ala Pro Ala Glu Arg Val Asp Val Trp Val Asp Phe Ser Arg Trp Pro
325     330     335
Val Gly Thr Lys Leu Thr Leu Gln Ser Leu Ala Phe Asp Gly Val Leu
340     345     350
Ala Met Gly Gly Met Ile Gly Asn Thr Ser Leu Pro Ser Gly Ala Ser
355     360     365
Phe Pro Val Leu Lys Val Gly Val Asp Gln Arg Ala Asn Thr Lys Met
370     375     380
Glu Leu Pro Ala Arg Leu Ala Ser Leu Pro Pro Val Arg Pro Gln Asp

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385		390		395		400
Ala Val Asn Ala His	Asn Pro Lys Val Phe Asn Ile Thr Met Gly Met					
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Met Val Trp Gly Val Asn Gly Arg Arg Phe Glu Met Asn Gly Val Ala						
	420		425		430	
Lys Thr Glu Thr Val Arg Arg Asn Ser Thr Glu Ile Trp Glu Phe Arg						
	435		440		445	
Asn Glu Glu Ser Met Met Leu Met Ala His Ser Met His Val His Gly						
	450		455		460	
Leu Gln Phe Arg Val Leu Glu Arg Thr Val Gln Pro Asp Phe Arg Ala						
	465		470		475	
Gly Tyr Arg Thr Leu Ala Ala Gly Leu Val Asp Asp Gly Trp Lys Asp						
	485		490		495	
Thr Val Leu Leu Met Pro Gly Glu Arg Ile Arg Leu Leu Leu Arg Phe						
	500		505		510	
Ala Ser Tyr Thr Gly Leu Phe Leu Tyr His Cys His Met Leu Glu His						
	515		520		525	
Glu Asp Ser Gly Leu Met Arg Asn Tyr Leu Ile Gln Thr						
	530		535		540	

<210> 5

<211> 1584

<212> DNA

<213> Bacteria

<400> 5

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agcggaaatt	tgagtaaaca	atccctcaat	atccccgat	acttcctttt	tcccgatgga	180
cagcgagtaa	gtataaccgc	aaagtggaca	acccttgagg	taatccccgg	aaagtgcagc	240
gatatgctcg	tttacgagat	tgataatgag	tacaaccccg	tcataatttct	cagaaagggg	300
caaactttca	gtgctgactt	tgtgaataac	tccggagaag	actcaataat	acactggcac	360
ggcttttagag	ctccctggaa	gtccgacgga	catccctatt	acgccgtaaa	agacggagaa	420
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cacccccacg	gaaggacggg	ttatcagggt	tactacggtc	ttgcgggaat	gataataatc	540
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atgggacaca	tgggcttctg	gggagacact	attctcgtga	acttaacgcc	aaacccttat	720
atggacgtag	agagaaaagat	ttacagggtc	agaattttga	acggttctaa	tgcacggccc	780
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ccgcaggaca	taaacaatcc	gaagggttct	tttgaacaga	acaacggcga	cgtgggtgatt	1320
atagagtacg	taaacaacac	gggtatgtac	caccccatgc	acatacacgg	ctttcagttt	1380
caagttctag	aaaggagctt	gggacctttg	agggtctacg	acctcggtcg	gaaggatacg	1440
gtaatatgtag	ctcccatgga	aacggtaaga	atagcggtgg	acatgagcca	tccctataac	1500
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<210> 6

<211> 527

<212> PRT

<213> Bacteria

<220>

<221> SIGNAL

<222> (1)...(37)

<221> DOMAIN

<222> (56)...(185)

<223> Multicopper oxidase

<400> 6

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Met Asp Arg Arg Lys Phe Ile Lys Thr Ser Leu Phe Ser Ala Leu Gly
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      20      25      30
Thr Gly Ser Ser Ser Gly Gln Gly Ser Gly Thr Leu Ser Lys Gln Ser
      35      40      45
Leu Asn Ile Pro Gly Tyr Phe Leu Phe Pro Asp Gly Gln Arg Val Ser
      50      55      60
Ile Thr Ala Lys Trp Thr Thr Leu Glu Val Ile Pro Gly Lys Ser Thr
      65      70      75      80
Asp Met Leu Val Tyr Glu Ile Asp Asn Glu Tyr Asn Pro Val Ile Phe
      85      90      95
Leu Arg Lys Gly Gln Thr Phe Ser Ala Asp Phe Val Asn Asn Ser Gly
      100      105      110
Glu Asp Ser Ile Ile His Trp His Gly Phe Arg Ala Pro Trp Lys Ser
      115      120      125
Asp Gly His Pro Tyr Tyr Ala Val Lys Asp Gly Glu Thr Tyr Ser Tyr
      130      135      140
Pro Asp Phe Thr Ile Ile Asp Arg Ser Gly Thr Tyr Phe Tyr His Pro
      145      150      155      160
His Pro His Gly Arg Thr Gly Tyr Gln Val Tyr Tyr Gly Leu Ala Gly
      165      170      175
Met Ile Ile Ile Glu Asp Glu Asp Glu Asp Asn Leu Lys Gln Ala Leu
      180      185      190
Asp Leu Glu Tyr Gly Val Ile Asp Ile Pro Leu Ile Ile Gln Asp Lys
      195      200      205
Thr Phe Asp Ser Ser Gly Gln Leu Val Tyr Asn Pro Met Gly His Met
      210      215      220
Gly Phe Trp Gly Asp Thr Ile Leu Val Asn Leu Thr Pro Asn Pro Tyr
      225      230      235      240
Met Asp Val Glu Arg Lys Ile Tyr Arg Phe Arg Ile Leu Asn Gly Ser
      245      250      255
Asn Ala Arg Pro Tyr Arg Leu Ala Leu Leu Arg Gly Asn Gln Arg Met
      260      265      270
Arg Phe Trp Val Ile Gly Val Glu Gly Gly Leu Leu Asp Thr Pro Lys
      275      280      285
Glu Val Asn Glu Ile Leu Val Ala Pro Gly Glu Arg Ile Asp Ile Leu
      290      295      300
Val Asp Phe Arg Asp Ala Ser Val Asn Asp Val Ile Lys Leu Tyr Asn
      305      310      315      320
Phe Pro His Asn Leu Ile Gly Met Gly Met Ile Gly Met Arg Met Gly
      325      330      335
Met Gly Met Glu Arg Gly Met Gly Met Gly Asn Gly Met Asn Met Asp
      340      345      350
Met Gly Met Ala Asp Asn Ser Glu Phe Glu Val Met Glu Phe Arg Val
      355      360      365
Thr Lys Asp Ser Ala Tyr Asp Lys Ser Ile Pro Gln Arg Leu Ser Glu
      370      375      380
Val Thr Pro Ile Asn Thr Asp Gly Ala Gln Val Gln Arg Ile Thr Leu
      385      390      395      400

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<210> 8
<211> 491
<212> PRT
<213> Unknown

<220>
<223> Obtained from an environmental sample
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<221> SIGNAL

<222> (1)...(31)

<221> DOMAIN

<222> (190)...(336)

<223> Multicopper oxidase

<400> 8

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Met Asp Gly Phe Val Glu Ser Arg Arg Glu Phe Leu Arg Thr Thr Gly
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Met Thr Ala Gly Ala Met Leu Phe Ser Ser Gln Asn Leu Phe Ala Ala
          20          25          30
Ala Ala Glu Ala Ala Ala Asp Tyr Thr Val Arg Ile Lys Ala Ala Pro
          35          40          45
Ile Glu Ile Ala Ser Asp Lys Ile Leu Ser Thr Ile Thr Tyr Asn Gly
          50          55          60
Gln Phe Pro Gly Pro Leu Ile Arg Leu Lys Glu Gly Arg Gln Val Thr
          65          70          75          80
Val Asp Ile Phe Asn Glu Thr Asp Thr Pro Glu Gln Leu His Trp His
          85          90          95
Gly Gln Phe Val Ser Pro Asp Val Asp Gly Ala Ala Glu Glu Gly Thr
          100          105          110
Pro Tyr Ile Pro Ala His Gly Gln Arg Arg Ile Met Phe Thr Pro Gly
          115          120          125
Pro Ala Gly Leu Arg Phe Tyr His Thr His Asn Arg Ala Gly Ala Asp
          130          135          140
Leu Ser Leu Gly Gln Tyr Ser Gly Gln Val Gly Pro Val Tyr Ile Glu
          145          150          155          160
Pro Lys Glu Asn Pro Gly Arg Tyr Asp Arg Glu Val Phe Leu Val Leu
          165          170          175
Lys Glu Phe Glu Pro Thr Leu Ser Arg Gly Gly Asp Met Pro Gln Asp
          180          185          190
Phe Leu Ser Pro Ser Ala Ile Asp Lys Thr Leu Lys Glu Thr Gly Glu
          195          200          205
Ala Ala Met Lys Ala Ser Leu Ala Lys Arg Met Pro His Gly Tyr Glu
          210          215          220
Val Gly Tyr Lys Phe Phe Thr Ile Asn Gly Arg Met Leu Gly His Gly
          225          230          235          240
Glu Pro Ile Arg Val Lys His Gly Glu Arg Val Leu Phe His Ile Leu
          245          250          255
Asn Gly Ser Ala Thr Glu Ile Arg Ser Leu Ala Leu Pro Asp His Ser
          260          265          270
Phe Glu Val Ile Ala Leu Asp Gly Asn Pro Val Pro Asn Pro Val His
          275          280          285
Val Pro Val Leu Trp Leu Gly Thr Ala Glu Arg Ile Ser Ala Val Val
          290          295          300
Glu Met Asn His Pro Gly Val Trp Ile Leu Gly Asp Leu Ala Asp Asp
          305          310          315          320
Asp Arg Asn His Gly Met Gly Val Val Val Glu Tyr Ala Gly Arg Ser
          325          330          335
Gly Lys Pro His Trp Ala Thr Pro Pro Phe Arg Trp Asp Tyr Ala
          340          345          350
Arg Phe Ala Lys Pro Asn Ala Ser Ala Pro Glu Ala Asp Glu Ala Phe
          355          360          365
Asp Met Thr Phe Ala Lys Asp Asn Ala Ala Glu Ala Gly Phe Asn Arg
          370          375          380
Trp Thr Ile Asn Gly Val Ala Tyr Pro Met Ser Asn Glu Met Ala Pro
          385          390          395          400

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Ala	Ser	Phe	His	Leu	Arg	Gln	Gly	Lys	Arg	Tyr	Arg	Leu	Arg	Met	Arg
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Asn	Ala	Ser	Asp	Ile	His	Pro	Ile	His	Leu	His	Arg	His	Ser	Phe	
			420				425					430			
Glu	Leu	Ala	Asn	Leu	Ala	Gly	Thr	Lys	Thr	Ala	Gly	Val	Met	Lys	Asp
			435				440					445			
Val	Val	Met	Leu	Gly	Gly	Tyr	Gln	Gln	Leu	Glu	Ile	Asp	Phe	Val	Ala
	450				455						460				
Asp	Asn	Pro	Gly	Leu	Thr	Leu	Phe	His	Cys	His	Gln	Gln	Leu	His	Met
465					470				475						480
Asp	Phe	Gly	Phe	Met	Ala	Leu	Phe	Asp	Tyr	Val					
			485						490						

<210> 9

<211> 1293

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 9

atggtgtctc	gtcgaaattt	tctcagcggc	tccggcgccg	cggtgttggg	ggcggcactg	60
gtcagcaagg	ccggcgccgc	atcattgccc	gaggcgccca	cgatgaccac	ggccgcgatg	120
cagccaccgc	tcgtgcccc	ggctgggagg	ccatacacgc	ccgttgccac	ggtgaacggc	180
tggctcgtgc	cgtggcgcat	gaagaacggc	tgggaaggagt	ttcatctgat	tgccgagccg	240
gtggtgcgcg	aactcgcgcc	gggcatgagt	gctcatctgt	ggggctataa	cggtcaggcg	300
ccggggccga	ccatcgaggc	cggtgaaggc	gacaagggtc	gcatcttcgt	gaccaacagg	360
ctgccggagt	acaccacggg	tactggcat	ggcatgctcc	tgccgtgcgg	catggacggc	420
gtcggcggtc	tcacgcagcc	gcataattcc	ccgggcaaga	cctttgttta	cgagtttcag	480
ctcgagaagc	acggcacggt	catgtatcac	ccgcacgccg	acgagatggt	gcagatggcg	540
atgggcatga	tgggcagctt	catcgttcat	ccgaaggacc	cgggcgtcat	gcgggtggat	600
cgcgacttcg	tgttcacat	gtccgcgtac	gacatcgacc	caggcagctt	cacgccgcgc	660
gtgaacgaga	tgaccgactt	caacatatgg	acgtggaatg	cccgcgtgtt	tccgggtatc	720
gatgcgttgc	cggcgcgcg	ggcgatcg	gtgcgcattc	gcgtcggcaa	tctgacgatg	780
accaatcacc	cgatccacct	gcacggctac	cagttcgaag	tgggtgggaac	ggacggcgga	840
tggattcaac	cctcggcgcg	ctggccggag	gtgaccgcgg	atgtcgcggt	cggccagatg	900
cgcgcgatcg	agttcaccgc	gaaccggccc	ggcgactggg	cgtttcattg	ccacaaatcc	960
catcacacga	tgaatcgcat	ggggcaccag	gtgccgaacc	tgatcggcgt	gccgcagcag	1020
gacctcgca	aacgtatcaa	caggctgggtg	cccgattaca	tggcgatggg	cagcacgggc	1080
ggttcaatgg	ggggcatgga	aatgccgcta	cccgataaca	cgttgccgat	gatggccggc	1140
acggggccgt	tcggcgcgct	ggaaatgggc	ggcatgttca	gcgtcgtgaa	agtgcgggag	1200
gggttggggc	gcaacgacta	tcgcgacccg	gggtggttca	ggcatccgca	aggaaccgtg	1260
gcgtacgaat	acaccggcga	actgcctggt	tga			1293

<210> 10

<211> 430

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<221> SIGNAL

<222> (1)...(26)

<221> DOMAIN

<222> (199)...(343)

<223> Multicopper oxidase

<400> 10

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Met Val Ser Arg Arg Asn Phe Leu Ser Gly Ser Gly Ala Ala Leu Leu
 1      5      10      15
Gly Ala Ala Leu Val Ser Lys Ala Gly Ala Ala Ser Leu Pro Glu Ala
 20      25      30
Pro Thr Met Thr Thr Ala Ala Met Gln Pro Pro Leu Val Pro Pro Ala
 35      40      45
Gly Arg Pro Tyr Thr Pro Val Ala Thr Leu Asn Gly Trp Ser Leu Pro
 50      55      60
Trp Arg Met Lys Asn Gly Trp Lys Glu Phe His Leu Ile Ala Glu Pro
 65      70      75      80
Val Val Arg Glu Leu Ala Pro Gly Met Ser Ala His Leu Trp Gly Tyr
 85      90      95
Asn Gly Gln Ala Pro Gly Pro Thr Ile Glu Ala Val Glu Gly Asp Lys
100      105      110
Val Arg Ile Phe Val Thr Asn Arg Leu Pro Glu Tyr Thr Thr Val His
115      120      125
Trp His Gly Met Leu Leu Pro Cys Gly Met Asp Gly Val Gly Gly Leu
130      135      140
Thr Gln Pro His Ile Pro Pro Gly Lys Thr Phe Val Tyr Glu Phe Gln
145      150      155      160
Leu Glu Lys His Gly Thr Phe Met Tyr His Pro His Ala Asp Glu Met
165      170      175
Val Gln Met Ala Met Gly Met Met Gly Ser Phe Ile Val His Pro Lys
180      185      190
Asp Pro Gly Val Met Arg Val Asp Arg Asp Phe Val Phe Ile Met Ser
195      200      205
Ala Tyr Asp Ile Asp Pro Gly Ser Phe Thr Pro Arg Val Asn Glu Met
210      215      220
Thr Asp Phe Asn Ile Trp Thr Trp Asn Ala Arg Val Phe Pro Gly Ile
225      230      235      240
Asp Ala Leu Pro Val Arg Ala Gly Asp Arg Val Arg Ile Arg Val Gly
245      250      255
Asn Leu Thr Met Thr Asn His Pro Ile His Leu His Gly Tyr Gln Phe
260      265      270
Glu Val Val Gly Thr Asp Gly Gly Trp Ile Gln Pro Ser Ala Arg Trp
275      280      285
Pro Glu Val Thr Ala Asp Val Ala Val Gly Gln Met Arg Ala Ile Glu
290      295      300
Phe Thr Ala Asn Arg Pro Gly Asp Trp Ala Phe His Cys His Lys Ser
305      310      315      320
His His Thr Met Asn Ala Met Gly His Gln Val Pro Asn Leu Ile Gly
325      330      335
Val Pro Gln Gln Asp Leu Ala Lys Arg Ile Asn Arg Leu Val Pro Asp
340      345      350
Tyr Met Ala Met Gly Ser Thr Gly Gly Ser Met Gly Gly Met Glu Met
355      360      365
Pro Leu Pro Asp Asn Thr Leu Pro Met Met Ala Gly Thr Gly Pro Phe
370      375      380
Gly Ala Leu Glu Met Gly Gly Met Phe Ser Val Val Lys Val Arg Glu
385      390      395      400
Gly Leu Gly Arg Asn Asp Tyr Arg Asp Pro Gly Trp Phe Arg His Pro
405      410      415
Gln Gly Thr Val Ala Tyr Glu Tyr Thr Gly Glu Leu Pro Gly
420      425      430

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<210> 11

<211> 1338

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 11

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atgccgcgct ctctccagta cttcgtcgcc ttcaccggga tgggcaccct cttcgccgcc      60
acgtgtgtgc tggcggeget cgccctcgga gacggctcag ctgcccgcag caccgacagc      120
acccccagcc cggcttccgc cgagcagccc gacgacgggc aaccgatcgg cgccatcgag      180
atccgtgcct tcgacgtcgg gttcgagccg acgtccatca gcgtcgagcg accggggcgc      240
tacaccgtca ccttcgtcaa cgacggcggc gccttccacg acctggtttt cgcggacggc      300
accaccctcg aggcgcgcgc gcgtgagacg gtcagcgggc aggtcgtcat ccccgccgag      360
gggctgacct acatctgtct ggttcccggc cagccgacg ccggcatgcg cggcgagggtg      420
atggtcggcg acgatccgca tgctggccat ccgccacagc agccgctgac tgcggaggag      480
atgagggaca aggatgcggc ccgcacggcg ctcttccctg ccgaaacgga gggcaagggg      540
ggcgtgccac tcgagccgac cgtcctcgag gacggaacgc tggagtggga gctgaccgcc      600
tccgagatcg agtgggagac cgagcccgga gtctggctga attccatggc ctacaacggc      660
atggttcccc gtcccagact gcgcgcgagc gtgggcgacc gggcgcgcat catcctgcac      720
aacgagctca gcgagccgac caccatccac ttccacggcc tgctcgtgcc gaacgcgatg      780
gacggcgtgc ccctcatcaa ccaggaagcg gtactgcccg gcgagtcatt cacctacgag      840
ttcgagatcc gcaatgccgg ctcgcacatg taccacagcc acttcatggc cgagcaccag      900
gtaccgatgg gcctgtctcg ggcattcatc accaccgatc cgaacgacga ggccgatccg      960
gcggccgaca tcgactacac gatgatcctc aacgacgggc cgctcggcta cagatcaaac     1020
ggcaagggct tcccggccac agagccgata gtggccgagt tcggccagac gatccgcgtg     1080
cgctacatga acgagggact gcagatccac ccgatgcacc tgcacggcat cgctcagcag     1140
gtgatcgcgc gcgacggcta ccttgtgccg caccgcgtact acgaggacac cgtcctgggt     1200
tcgcccggcg agcgggtcga cgtcctgata gaggccaacg agctcggcgt gtgggccttc     1260
cactgccatg tgctgacca cgccgagggg ccggatggca tgttcggaat ggtgaccgcg     1320
ctcatcgtcc aggagtga

```

<210> 12

<211> 445

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<221> SIGNAL

<222> (1)...(47)

<221> DOMAIN

<222> (322)...(445)

<223> Multicopper oxidase

<221> DOMAIN

<222> (55)...(143)

<223> Copper binding proteins, plastocyanin/azurin family

<400> 12

```

Met Pro Arg Ser Leu Gln Tyr Phe Val Ala Phe Thr Gly Met Gly Thr
 1              5              10              15
Leu Phe Ala Ala Thr Leu Leu Leu Ala Ala Leu Ala Leu Gly Asp Gly
      20              25              30
Ser Ala Ala Arg Ser Thr Asp Ser Thr Pro Ser Pro Ala Ser Ala Glu
      35              40              45
Gln Pro Asp Asp Gly Gln Pro Ile Gly Ala Ile Glu Ile Arg Ala Phe

```

50	55	60
Asp Val Gly Phe Glu Pro Thr Ser Ile Ser Val Glu Arg Pro Gly Arg		
65	70	75
Tyr Thr Val Thr Phe Val Asn Asp Gly Gly Ala Phe His Asp Leu Val		80
	85	90
Phe Ala Asp Gly Thr Thr Leu Glu Ala Ala Ala Arg Glu Thr Val Ser		95
	100	105
Gly Glu Val Val Ile Pro Ala Glu Gly Leu Thr Tyr Ile Cys Ser Val		110
	115	120
Pro Gly His Ala Asp Ala Gly Met Arg Gly Glu Val Met Val Gly Asp		125
	130	135
Asp Pro His Ala Gly His Pro Pro Gln Gln Pro Leu Thr Ala Glu Glu		140
	145	150
Met Arg Asp Lys Asp Ala Ala Arg Thr Ala Leu Phe Pro Ala Glu Thr		155
	165	170
Glu Gly Lys Gly Gly Val Pro Leu Glu Pro Thr Val Leu Asp Asp Gly		175
	180	185
Thr Leu Glu Trp Glu Leu Thr Ala Ser Glu Ile Glu Trp Glu Thr Glu		190
	195	200
Pro Gly Val Trp Leu Asn Ser Met Ala Tyr Asn Gly Met Val Pro Gly		205
	210	215
Pro Glu Leu Arg Ala Glu Val Gly Asp Arg Val Arg Ile Ile Leu His		220
	225	230
Asn Glu Leu Ser Glu Pro Thr Thr Ile His Phe His Gly Leu Leu Val		235
	245	250
Pro Asn Ala Met Asp Gly Val Pro Leu Ile Asn Gln Glu Ala Val Leu		255
	260	265
Pro Gly Glu Ser Phe Thr Tyr Glu Phe Glu Ile Arg Asn Ala Gly Ser		270
	275	280
His Met Tyr His Ser His Phe Met Ala Glu His Gln Val Pro Met Gly		285
	290	295
Leu Leu Gly Ala Phe Ile Thr Thr Asp Pro Asn Asp Glu Ala Asp Pro		300
	305	310
Ala Ala Asp Ile Asp Tyr Thr Met Ile Leu Asn Asp Gly Pro Leu Gly		315
	325	330
Tyr Thr Ile Asn Gly Lys Gly Phe Pro Ala Thr Glu Pro Ile Val Ala		335
	340	345
Glu Phe Gly Gln Thr Ile Arg Val Arg Tyr Met Asn Glu Gly Leu Gln		350
	355	360
Ile His Pro Met His Leu His Gly Ile Ala Gln Gln Val Ile Ala Arg		365
	370	375
Asp Gly Tyr Leu Val Pro His Pro Tyr Tyr Glu Asp Thr Val Leu Val		380
	385	390
Ser Pro Gly Glu Arg Val Asp Val Leu Ile Glu Ala Asn Glu Leu Gly		395
	405	410
Val Trp Ala Phe His Cys His Val Leu Thr His Ala Glu Gly Pro Asp		415
	420	425
Gly Met Phe Gly Met Val Thr Ala Leu Ile Val Gln Glu		430
	435	440
		445

<210> 13

<211> 1452

<212> DNA

<213> Bacteria

<400> 13

atgacggccg	cgggggccgc	cctcaccgcg	agcggactcc	tcatcagccg	gacctcgctc	60
agcgacaccc	gggcccggcg	cccggcgggc	gcctcgccgt	tcgccgccca	gccggtggcc	120
gcccgagccc	tcgccccgat	cgtcacgccc	ttccgcaccg	ccatgcccac	cccgcgggtg	180

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gcccgcgcgg tctccgtcac ctgcaccacc gacacgtaca gcatcccggg caccagacc 240
acggcgagaga tcatccccgg ggcccgacc cccgtcctca cctacggcgg cagcttcccc 300
ggccccacca tcaaggcgcg ctccggtcgg cgcgtggtcg tcaagcagcc caaccggatc 360
accaccggca cctccatgca cctgcacgga gcggtcgtcg accccgcca cgcacggcggc 420
cccatggacc tgatcacgcc cggcggggcag cgcacgtaca cctaccccaa cccgcagggtg 480
gcggccaccc tctggtacca cgaccacgcc caccacatgg aggcagagca cgtctaccgc 540
ggcatgtcgg gcttctacct gatatccgac gacaacgagg acgcgctgcc cctgccgcgc 600
ggcacctacg acgtgccgat cgtcgttcgc gacatcgggc tcaacccga cggcacccctc 660
ttcttcgacc acaacttcga cacccgggcg cagatcctgg tcaacggcaa gccgcagccc 720
tacttcagg tcgcccggcg caagtaccgg ctgcgcaccc tcaacggctc caaccagcgg 780
cccttcgagt tccggtcttc cgacggcggc gattcaccc agatcgctc cgaccgcggc 840
ctgctccccg ccccgtagac gacgacgacc ctgccgtctc cgccggccga acgggcccgc 900
atcgtcgtcg acttctcgcg ctaccccggtg ggcagcagcg tcgtcctgga gaacgcctac 960
ttcccgagac cctccaacaa ggagatcctc cgcttcgacg tcgtccgctc cgcctacgac 1020
cccagctcgg tcccggcccc gctcgccacc ctgccgccga ccgccgcgcc gaccagacg 1080
cgcaactaca cgctcgactt cgacgtgcag accggcgcgg gctcgatcag cggcaagacc 1140
tgggacgagc agcgcgtcga caccacggtg cgccaggggg acaccgaggt ctgggagatc 1200
aagaacaccc accccttcac cccgcacaac ttccacatcc acctggtgga cttccggatc 1260
ctcgacatcg acggcaagcc gccgacgccc ggcgacgccc gactcaagga caccgtccgg 1320
atcggggccg gggagacggc ccgcatectc gtccacttcg acttcccgtc ctggggccgc 1380
tactactacc actgccacct gatcgaccac tcgtcgatgg gcatgatggc caacctggag 1440
atcacccgat ga 1452

```

<210> 14

<211> 483

<212> PRT

<213> Bacteria

<220>

<221> SIGNAL

<222> (1)...(21)

<400> 14

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Met Thr Ala Ala Gly Ala Ala Leu Thr Ala Ser Gly Leu Leu Ile Ser
 1          5          10          15
Arg Thr Ser Leu Ser Asp Thr Arg Ala Gly Gly Pro Ala Gly Ala Ser
 20          25          30
Pro Phe Ala Ala Gln Pro Val Ala Ala Gln Ala Leu Ala Pro Ile Val
 35          40          45
Thr Pro Phe Arg Thr Ala Met Pro Ile Pro Pro Val Ala Arg Pro Val
 50          55          60
Ser Val Thr Ser Thr Thr Asp Thr Tyr Ser Ile Pro Val Thr Gln Thr
 65          70          75          80
Thr Ala Glu Ile Ile Pro Gly Val Arg Thr Pro Val Leu Thr Tyr Gly
 85          90          95
Gly Ser Phe Pro Gly Pro Thr Ile Lys Ala Arg Ser Gly Arg Arg Val
 100         105         110
Val Val Lys Gln Pro Asn Arg Ile Thr Thr Gly Thr Ser Met His Leu
 115         120         125
His Gly Ala Val Val Asp Pro Ala Asn Asp Gly Gly Pro Met Asp Leu
 130         135         140
Ile Thr Pro Gly Gly Gln Arg Thr Tyr Thr Tyr Pro Asn Pro Gln Val
 145         150         155         160
Ala Ala Thr Leu Trp Tyr His Asp His Ala His His Met Glu Ala Glu
 165         170         175
His Val Tyr Arg Gly Met Ser Gly Phe Tyr Leu Ile Ser Asp Asp Asn
 180         185         190
Glu Asp Ala Leu Pro Leu Pro Arg Gly Thr Tyr Asp Val Pro Ile Val
 195         200         205

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Val Arg Asp Ile Gly Leu Asn Pro Asp Gly Thr Leu Phe Phe Asp His
 210 215 220
 Asn Phe Asp Thr Arg Pro Gln Ile Leu Val Asn Gly Lys Pro Gln Pro
 225 230 235 240
 Tyr Phe Gln Val Ala Ala Arg Lys Tyr Arg Leu Arg Ile Leu Asn Gly
 245 250 255
 Ser Asn Gln Arg Pro Phe Glu Phe Arg Leu Ser Asp Gly Gly Glu Phe
 260 265 270
 Thr Gln Ile Ala Ser Asp Arg Gly Leu Leu Pro Ala Pro Tyr Thr Thr
 275 280 285
 Thr Thr Leu Pro Leu Ser Pro Ala Glu Arg Ala Asp Ile Val Val Asp
 290 295 300
 Phe Ser Arg Tyr Pro Val Gly Ser Ser Val Val Leu Glu Asn Ala Tyr
 305 310 315 320
 Phe Pro Glu Pro Ser Asn Lys Glu Ile Leu Arg Phe Asp Val Val Arg
 325 330 335
 Ser Ala Tyr Asp Pro Ser Ser Val Pro Ala Arg Leu Ala Thr Leu Pro
 340 345 350
 Pro Thr Ala Ala Pro Thr Gln Thr Arg Asn Tyr Thr Leu Asp Phe Asp
 355 360 365
 Val Gln Thr Gly Ala Gly Ser Ile Ser Gly Lys Thr Trp Asp Glu Gln
 370 375 380
 Arg Val Asp Thr Thr Val Arg Gln Gly Asp Thr Glu Val Trp Glu Ile
 385 390 395 400
 Lys Asn Thr His Pro Phe Ile Pro His Asn Phe His Ile His Leu Val
 405 410 415
 Asp Phe Arg Ile Leu Asp Ile Asp Gly Lys Pro Pro Thr Pro Gly Asp
 420 425 430
 Ala Gly Leu Lys Asp Thr Val Arg Ile Gly Pro Gly Glu Thr Ala Arg
 435 440 445
 Ile Leu Val His Phe Asp Phe Pro Tyr Ser Gly Arg Tyr Tyr Tyr His
 450 455 460
 Cys His Leu Ile Asp His Ser Ser Met Gly Met Met Ala Asn Leu Glu
 465 470 475 480
 Ile Thr Arg

<210> 15

<211> 1542

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 15

atgacacttg	aaaaatttgt	ggatgctctc	ccaatcccag	atacactaaa	gccggtacag	60
cagtcaaaaag	atagcacata	ctacgaagta	accatggagg	aatgctacca	tcagcttcac	120
cgcgatctcc	ctccaacccg	cttgtggggc	tataacgggt	tattccccgg	tcccaccatt	180
aaggccaaaa	gaaatgaaaa	cgtttatgtg	aagtggatga	ataaccttcc	ttcagagcat	240
tttcttccga	ttgatcacac	cattcatcac	agtgcagcc	agcatgccga	acccgaggtg	300
aaaaccgtcg	ttcatttaca	cggcggcgctc	actccagatg	acagcgacgg	ttatcctgag	360
gcctggtttt	ctaaagactt	tgaacaaaca	ggcccttatt	ttaaacgaga	ggtttaccat	420
tatccaaatc	agcagcgcg	agctatttta	tggtatcacg	atcatgctat	ggcgctcacg	480
aggetgaatg	tgtatgccgg	gctcatcggt	gcttatatca	tccatgaacc	aaaggaaaaa	540
cgctgaagc	tcccatcagg	tgaatacga	gtgccgcttt	tgatcacgga	ccgtacgatt	600
aatgaagatg	gctctttatt	ttatccgagc	ggaccggaaa	acccttcacc	gtcactgcct	660
aatccgctca	tcgttccagc	cttttgcgga	gatacaattc	tcgtcaacgg	gaaggcatgg	720
ccatacatgg	aggtcgaacc	gagaaaatac	cgcttccg	tcataaatgc	ctctaatac	780

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agaacatata acctgtcact tgataatggt ggagaattta tccagatcgg ttctgacggc      840
ggacttttgc cgcgctccgt catgctaaac tctttcagta tcgcgccagc tgagcgcttt      900
gatatcctca ttgacttcgc cgcggttgaa ggacaatcga ttatttttagc aaacagcgag      960
ggctgcggcg gcgacgttaa tccggaaaca gacgcaaaca tcatgcaatt cagagtcaca     1020
aaaccgttag cccaaaaaga cgaaagcaga aagccaaaat acctggcatc ttacccttca     1080
gtacagcacg aaagaatata aaacctccga acattgaagc tggcaggaac tcaagatcaa     1140
tacggcagac ccgttcttct tcttaacaac aaacgctggc acgatcctgt cactgaagca     1200
ccgaaagccg gttctaccga aatatggctg atcatcaatc cgacacgcgg aacacatccc     1260
atccatcttc atttggcttc ctcccggtga ttggaccggc gccatttga tacagcccgt     1320
tttgaagagc gcggagaact ggcctacacc ggaccgcggc ttccgccgcc accaagtga     1380
aaaggctgga aagacacggg tcagtcccac gccggtgaag tcctgagaat cgccgtaaca     1440
ttcgggccat acactgggcg gtacgtatgg cattgccaca ttcttgagca tgaagactat     1500
gacatgatga gaccgatgga tgtgattgac ccccataaat aa                        1542

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<210> 16

<211> 513

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 16

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Met Thr Leu Glu Lys Phe Val Asp Ala Leu Pro Ile Pro Asp Thr Leu
1          5          10          15
Lys Pro Val Gln Gln Ser Lys Asp Ser Thr Tyr Tyr Glu Val Thr Met
20          25          30
Glu Glu Cys Tyr His Gln Leu His Arg Asp Leu Pro Pro Thr Arg Leu
35          40          45
Trp Gly Tyr Asn Gly Leu Phe Pro Gly Pro Thr Ile Lys Ala Lys Arg
50          55          60
Asn Glu Asn Val Tyr Val Lys Trp Met Asn Asn Leu Pro Ser Glu His
65          70          75          80
Phe Leu Pro Ile Asp His Thr Ile His His Ser Asp Ser Gln His Ala
85          90          95
Glu Pro Glu Val Lys Thr Val Val His Leu His Gly Gly Val Thr Pro
100          105          110
Asp Asp Ser Asp Gly Tyr Pro Glu Ala Trp Phe Ser Lys Asp Phe Glu
115          120          125
Gln Thr Gly Pro Tyr Phe Lys Arg Glu Val Tyr His Tyr Pro Asn Gln
130          135          140
Gln Arg Gly Ala Ile Leu Trp Tyr His Asp His Ala Met Ala Leu Thr
145          150          155          160
Arg Leu Asn Val Tyr Ala Gly Leu Ile Gly Ala Tyr Ile Ile His Glu
165          170          175
Pro Lys Glu Lys Arg Leu Lys Leu Pro Ser Gly Glu Tyr Asp Val Pro
180          185          190
Leu Leu Ile Thr Asp Arg Thr Ile Asn Glu Asp Gly Ser Leu Phe Tyr
195          200          205
Pro Ser Gly Pro Glu Asn Pro Ser Pro Ser Leu Pro Asn Pro Ser Ile
210          215          220
Val Pro Ala Phe Cys Gly Asp Thr Ile Leu Val Asn Gly Lys Ala Trp
225          230          235          240
Pro Tyr Met Glu Val Glu Pro Arg Lys Tyr Arg Phe Arg Val Ile Asn
245          250          255
Ala Ser Asn Thr Arg Thr Tyr Asn Leu Ser Leu Asp Asn Gly Gly Glu
260          265          270
Phe Ile Gln Ile Gly Ser Asp Gly Gly Leu Leu Pro Arg Ser Val Met
275          280          285

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Leu Asn Ser Phe Ser Ile Ala Pro Ala Glu Arg Phe Asp Ile Leu Ile
 290 295 300
 Asp Phe Ala Ala Phe Glu Gly Gln Ser Ile Ile Leu Ala Asn Ser Glu
 305 310 315 320
 Gly Cys Gly Gly Asp Val Asn Pro Glu Thr Asp Ala Asn Ile Met Gln
 325 330 335
 Phe Arg Val Thr Lys Pro Leu Ala Gln Lys Asp Glu Ser Arg Lys Pro
 340 345 350
 Lys Tyr Leu Ala Ser Tyr Pro Ser Val Gln His Glu Arg Ile Gln Asn
 355 360 365
 Leu Arg Thr Leu Lys Leu Ala Gly Thr Gln Asp Gln Tyr Gly Arg Pro
 370 375 380
 Val Leu Leu Leu Asn Asn Lys Arg Trp His Asp Pro Val Thr Glu Ala
 385 390 395 400
 Pro Lys Ala Gly Ser Thr Glu Ile Trp Ser Ile Ile Asn Pro Thr Arg
 405 410 415
 Gly Thr His Pro Ile His Leu His Leu Val Ser Phe Arg Val Leu Asp
 420 425 430
 Arg Arg Pro Phe Asp Thr Ala Arg Phe Glu Glu Arg Gly Glu Leu Ala
 435 440 445
 Tyr Thr Gly Pro Ala Val Pro Pro Pro Pro Ser Glu Lys Gly Trp Lys
 450 455 460
 Asp Thr Val Gln Ser His Ala Gly Glu Val Leu Arg Ile Ala Val Thr
 465 470 475 480
 Phe Gly Pro Tyr Thr Gly Arg Tyr Val Trp His Cys His Ile Leu Glu
 485 490 495
 His Glu Asp Tyr Asp Met Met Arg Pro Met Asp Val Ile Asp Pro His
 500 505 510
 Lys

<210> 17
 <211> 1743
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 17
 ttggatgttg gcgggccggt cgactattac gagatcgcgg tgcgccagtt tcaacagcag 60
 atattgcctc cacctttacc ggccacaact gtgtggagtt atggctcgac gaaccattcc 120
 ggcactttta attatccggc ttccaccatc gaagccaaat ggaacacacc tgtgcgcgtg 180
 aagtggatca acgatctgaa agatctatcg agcggcgaat tcttaccgca cttgctgccg 240
 gttgatccga ctcttactg ggcgaatccg ccaggaggtc ttggcggccg tgacatgcgt 300
 cccgaattca caactactcc agatccatat agaggaccg tgccgatcgt cacgcatctg 360
 cacggcggac acaccagcca ggagagcgat ggctttacag aagcgtggta tctgccgacc 420
 gcaaccaata tccccgctgg attcgcgact gaaggtacct ggtacgatac tttcaaaaca 480
 caattttctca accagtgagg tgtgccctgg cagccaggct ctgcgatctt tcaatatgcc 540
 aacgaccagc gagcgagcac gctctggtat catgatcacg cgctcggcat gacgcgtttg 600
 aatgtctatg ccggaccggc ggggttttac ttgttgccg gtgggccaga cgatatggtt 660
 gtgggcactc tgcctggacc cgctcccgcg ttagacgatc cgagtggcat gaagtactac 720
 gagatccccc tcgcaatcca ggatcgctca ttcaacaaag atggttcctt gttctatccg 780
 gagagccggc gattctttga cggctttaag aaggcataca ttcccagacag cgacatctcc 840
 ccaatatgga atccggaatt cttcggcaaa gtaatggtgg tcaacggccg cagctggccc 900
 ttccttgaag ttgagccgcg ccgctatcgt ttccggctgc tgaatggatg caactctcgt 960
 ttcctgatcc tgaagttcag caatccgaat ttaagcttct ggcagattgg taatgacggc 1020
 gggttcttgc cggcgccagt gcaactctcg caactgctga tgtcgccggc agaacgggca 1080
 gatgtgatcg tagacttttc gcaattcacg ccaggcaccg aaatcatttt ggagaacact 1140


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ggtcctgatg agccgttcgg tgggggagcg ccagacagcg atttcgacag cgccaaggcg 1200
gacacaacgc ggcaggtgat gcaattcagg gtcgtgccgc tgacaacagc ggataacaagc 1260
acaccaccta atctcctcga gttgccggcg atcactgggtt tgggtgcagc aaccaacagc 1320
cggcaggttt cgctcaacga agaggactca gcagtgcgtg tcggtgtcgg accaagagct 1380
gcgctgcttg gtactctgga tagtgagggc gagccggaga ttagaggctg ggacgatgcg 1440
atcactgaaa acccggccct tggcagcatc gaggtatggg agattcaciaa cttcacagaa 1500
gacgcgcacc cgattcacat tcacgaggtg gcgtttgaag tggatcaatcg acagccgttc 1560
gagggatctg caagaggtcc ggaagtttgg gaaggaggat tcaaggatac agtgatcgca 1620
tatccggagg agatcacgcg cgtcaaggct catttcgatc tgccgggact atatgtttgg 1680
cactgtcaca tcgtggagca cgaggacaac gaaatgatgc gcccctactt cattggccccg 1740
tga

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<210> 18

<211> 580

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 18

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Met Asp Val Gly Gly Pro Val Asp Tyr Tyr Glu Ile Ala Val Arg Gln
 1          5          10          15
Phe Gln Gln Gln Ile Leu Pro Pro Pro Leu Pro Ala Thr Thr Val Trp
 20          25          30
Ser Tyr Gly Ser Thr Asn His Ser Gly Thr Phe Asn Tyr Pro Ala Phe
 35          40          45
Thr Ile Glu Ala Lys Trp Asn Thr Pro Val Arg Val Lys Trp Ile Asn
 50          55          60
Asp Leu Lys Asp Leu Ser Ser Gly Glu Phe Leu Pro His Leu Leu Pro
 65          70          75          80
Val Asp Pro Thr Leu His Trp Ala Asn Pro Pro Gly Gly Leu Gly Gly
 85          90          95
Arg Asp Met Arg Pro Glu Phe Thr Thr Thr Pro Asp Pro Tyr Arg Gly
100          105          110
Pro Val Pro Ile Val Thr His Leu His Gly Gly His Thr Ser Gln Glu
115          120          125
Ser Asp Gly Phe Thr Glu Ala Trp Tyr Leu Pro Thr Ala Thr Asn Ile
130          135          140
Pro Ala Gly Phe Ala Thr Glu Gly Thr Trp Tyr Asp Thr Phe Lys Thr
145          150          155          160
Gln Phe Leu Asn Gln Trp Gly Val Pro Trp Gln Pro Gly Ser Ala Ile
165          170          175
Phe Gln Tyr Ala Asn Asp Gln Arg Ala Ser Thr Leu Trp Tyr His Asp
180          185          190
His Ala Leu Gly Met Thr Arg Leu Asn Val Tyr Ala Gly Pro Ala Gly
195          200          205
Phe Tyr Leu Leu Arg Gly Gly Pro Asp Asp Met Val Val Gly Thr Leu
210          215          220
Pro Gly Pro Ala Pro Ala Leu Asp Asp Pro Ser Gly Met Lys Tyr Tyr
225          230          235          240
Glu Ile Pro Leu Ala Ile Gln Asp Arg Ser Phe Asn Lys Asp Gly Ser
245          250          255
Leu Phe Tyr Pro Asp Ser Arg Arg Phe Phe Asp Gly Phe Lys Lys Ala
260          265          270
Tyr Ile Pro Asp Ser Asp Ile Ser Pro Ile Trp Asn Pro Glu Phe Phe
275          280          285
Gly Lys Val Met Val Val Asn Gly Arg Ser Trp Pro Phe Leu Glu Val
290          295          300

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Glu Pro Arg Arg Tyr Arg Phe Arg Leu Leu Asn Gly Cys Asn Ser Arg
 305 310 315 320
 Phe Leu Ile Leu Lys Phe Ser Asn Pro Asn Leu Ser Phe Trp Gln Ile
 325 330 335
 Gly Asn Asp Gly Gly Phe Leu Pro Ala Pro Val Gln Leu Ser Gln Leu
 340 345 350
 Leu Met Ser Pro Ala Glu Arg Ala Asp Val Ile Val Asp Phe Ser Gln
 355 360 365
 Phe Thr Pro Gly Thr Glu Ile Ile Leu Glu Asn Thr Gly Pro Asp Glu
 370 375 380
 Pro Phe Gly Gly Gly Glu Pro Asp Ser Asp Phe Asp Ser Ala Lys Ala
 385 390 395 400
 Asp Thr Thr Arg Gln Val Met Gln Phe Arg Val Val Pro Leu Thr Thr
 405 410 415
 Ala Asp Thr Ser Thr Pro Pro Asn Leu Leu Glu Leu Pro Ala Ile Thr
 420 425 430
 Gly Leu Gly Ala Ala Thr Asn Thr Arg Gln Val Ser Leu Asn Glu Glu
 435 440 445
 Asp Ser Ala Val Leu Phe Gly Val Gly Pro Arg Ala Ala Leu Leu Gly
 450 455 460
 Thr Leu Asp Ser Glu Gly Glu Pro Glu Ile Arg Gly Trp Asp Asp Ala
 465 470 475 480
 Ile Thr Glu Asn Pro Ala Leu Gly Ser Ile Glu Val Trp Glu Ile His
 485 490 495
 Asn Phe Thr Glu Asp Ala His Pro Ile His Ile His Glu Val Ala Phe
 500 505 510
 Glu Val Val Asn Arg Gln Pro Phe Glu Gly Ser Ala Arg Gly Pro Glu
 515 520 525
 Val Trp Glu Gly Gly Phe Lys Asp Thr Val Ile Ala Tyr Pro Glu Glu
 530 535 540
 Ile Thr Arg Val Lys Ala His Phe Asp Leu Pro Gly Leu Tyr Val Trp
 545 550 555 560
 His Cys His Ile Val Glu His Glu Asp Asn Glu Met Met Arg Pro Tyr
 565 570 575
 Phe Ile Gly Pro
 580

<210> 19

<211> 1467

<212> DNA

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 19

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ctgcccgtgc	tttcaggctg	tccggacgcg	ttgttcggtt	acggcgctcg	cacacgtcgc	120
tccgccgacg	gacttctcga	caccgggctt	cggctgcgtt	tcagtcatac	ctgtatcggc	180
cacgaacagg	tttacacccg	cgcctacgac	ggccgtatcc	caggacccgt	gctccgcgtg	240
aaaccgggcg	acaccctcaa	gatccgcctg	atcaacgatt	tgccggatga	ggaggacggc	300
cacggccacg	caaagtccga	tgacgtcaac	gtccctcatg	gattcaatac	caccaacatc	360
cacacccacg	ggttgacagt	ctcgccgtct	ggcaattccg	acaatgtctt	cgtccagatt	420
ccgcccgga	cgcatttcga	ttacgaatac	aacatcccgg	cgaatcatcc	cgcaggaaca	480
tttttctacc	atccgcacaa	gcacggttcg	gtcaccaacc	agatgatggg	tggtatggcc	540
ggtgcgctga	ttgtcgaggg	agacatcgac	cgcgtaccgg	agatcgctgc	cgcgaaggac	600
tatatcttcc	tgttacagga	actgcgcttc	gaggaggacg	gccacgcgcc	ggcgcatttt	660
ccgttccacg	atcttgacaa	cctgatgttg	ttccgcacgg	tgaacgggca	ggtcaacccc	720
acgatttacc	ttcggccccg	cgaggtgcag	cgctggcgat	tcattccatgc	gggcgtcgaa	780

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cactatctgc ccctcgaatt ggatggacat tgcgtccacc aaatcgcgca ggacggcatc      840
gccttcgcgt cgcccgaaaga gacggacagc gtctttctca ccccggaac ccgtgctgac      900
gtactcgtgc gcggtggcca acccggcacg tattacctgc gcaaacaggc ctatgaccag      960
ggacgcggcg aggtccccga agacattatc gccaccgtcg tcgtgaccgg gccgccttcc     1020
tttatgcgcc ttccctgggt gctgccgacg cctgcgctgc accgcaccat tactgacgaa     1080
gaagtgaccg gttcgcgcag tatcgtcttt agtgtgcaac ccgcgccagc gggcgaaatg     1140
tttcgcgcgt ttctgattga cgggcatact ttttcgccgg accgggtcga tcactctatt     1200
ccgctcgggt ccgtcgagga atggacgggt atcaacaacc accgggaaga ccatcccttc     1260
cacatccacg tcaatgcctt tgaagtcacc cacctgaacg gtgaccggct cccgcgcca     1320
cgctggcacg atgtaatcaa cgtgcccccc ttcggcactg cgaccttccg taccgccttc     1380
gaagatttca cgggcaagtt cgtcctgcac tgccacctcc tcgtccacga agacctcggc     1440
atgatgcaga cggttgaagt cacctga                                     1467

```

<210> 20

<211> 488

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<221> SIGNAL

<222> (1)...(25)

<221> DOMAIN

<222> (201)...(339)

<223> Multicopper oxidase

<400> 20

```

Met Thr Thr Arg Arg Asp Phe Leu Lys Arg Ala Gly Leu Gly Leu Ala
 1          5          10          15
Ala Ala Ala Thr Leu Pro Val Leu Ser Gly Cys Pro Asp Ala Leu Phe
          20          25          30
Arg Tyr Gly Val Ala Thr Arg Arg Ser Ala Asp Gly Leu Leu Asp Thr
          35          40          45
Arg Leu Arg Leu Arg Phe Ser His Thr Cys Ile Gly His Glu Gln Val
 50          55          60
Tyr Thr Arg Ala Tyr Asp Gly Arg Ile Pro Gly Pro Val Leu Arg Val
 65          70          75          80
Lys Pro Gly Asp Thr Leu Lys Ile Arg Leu Ile Asn Asp Leu Pro Asp
          85          90          95
Glu Glu Asp Gly His Gly His Ala Lys Ser Asp Asp Val Asn Val Pro
          100          105          110
His Gly Phe Asn Thr Thr Asn Ile His Thr His Gly Leu His Val Ser
          115          120          125
Pro Ser Gly Asn Ser Asp Asn Val Phe Val Gln Ile Pro Pro Gly Thr
          130          135          140
His Phe Asp Tyr Glu Tyr Asn Ile Pro Ala Asn His Pro Ala Gly Thr
          145          150          155          160
Phe Phe Tyr His Pro His Lys His Gly Ser Val Thr Asn Gln Met Met
          165          170          175
Gly Gly Met Ala Gly Ala Leu Ile Val Glu Gly Asp Ile Asp Arg Val
          180          185          190
Pro Glu Ile Ala Ala Ala Lys Asp Tyr Ile Phe Leu Leu Gln Glu Leu
          195          200          205
Arg Phe Glu Glu Asp Gly His Ala Pro Ala His Phe Pro Phe His Asp
          210          215          220
Leu Asp Asn Leu Met Leu Phe Arg Thr Val Asn Gly Gln Val Asn Pro
          225          230          235          240

```

Thr Ile Tyr Leu Arg Pro Gly Glu Val Gln Arg Trp Arg Phe Ile His
 245 250 255
 Ala Gly Val Glu His Tyr Leu Pro Leu Glu Leu Asp Gly His Ser Leu
 260 265 270
 His Gln Ile Ala Gln Asp Gly Ile Ala Phe Arg Ser Pro Glu Glu Thr
 275 280 285
 Asp Ser Val Phe Leu Thr Pro Gly Asn Arg Ala Asp Val Leu Val Arg
 290 295 300
 Gly Gly Gln Pro Gly Thr Tyr Tyr Leu Arg Lys Gln Ala Tyr Asp Gln
 305 310 315 320
 Gly Arg Gly Glu Val Pro Glu Asp Ile Ile Ala Thr Val Val Val Thr
 325 330 335
 Gly Pro Pro Ser Phe Met Arg Leu Pro Trp Leu Leu Pro Thr Pro Ala
 340 345 350
 Leu His Arg Thr Ile Thr Asp Glu Val Thr Gly Ser Arg Ser Ile
 355 360 365
 Val Phe Ser Val Gln Pro Ala Pro Ala Gly Glu Met Phe Pro Arg Phe
 370 375 380
 Leu Ile Asp Gly His Thr Phe Ser Pro Asp Arg Val Asp His Ser Ile
 385 390 395 400
 Pro Leu Gly Ser Val Glu Glu Trp Thr Val Ile Asn Asn His Arg Glu
 405 410 415
 Asp His Pro Phe His Ile His Val Asn Ala Phe Glu Val Thr His Leu
 420 425 430
 Asn Gly Asp Arg Leu Pro Arg Pro Arg Trp His Asp Val Ile Asn Val
 435 440 445
 Pro Pro Phe Gly Thr Ala Thr Phe Arg Thr Arg Phe Glu Asp Phe Thr
 450 455 460
 Gly Lys Phe Val Leu His Cys His Leu Leu Val His Glu Asp Leu Gly
 465 470 475 480
 Met Met Gln Thr Val Glu Val Thr
 485

<210> 21
 <211> 1356
 <212> DNA
 <213> Unknown

<220>
 <223> Obtained from an environmental sample

<400> 21
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 gtcggccagt gcctgtgccc gggaccggga ggcctgagct tgctcgacaa ggcgacgaat 120
 tccggccaac gccgtctggt cgccgacggc gtcgaccgtg acccgcagtg ccgagtcgtg 180
 gccacggtgc ccgccaccac tcggtttcca gcagccttgg gcaccggccg ggactcacca 240
 gtgatcagcg ggctcgccga tgtcaccaat ctccacactc acggctttca tgtttcaccg 300
 caagggaact ccgacaacat cttcctccac atcaaccccg gcgagacctt cgactacgag 360
 ttcaagctgc ccgcaacca ctcaccgggg atgtactggg atcaccgcga tggtcacggc 420
 gacaccgccc cccagtgcga cggcggcatg gccggggtga tcctgatcga cggcggtctc 480
 gacgaggtgc cggaatcgc cggcttgacc gaacgcctgc tcgtcctcca ggcgacgcaa 540
 ttcgacggcg acggcaacct cgtcccttac aacaaccagt cgaacgcgac tcggcagcgc 600
 ttctgtcaacg gtcaactcaa cccaacgata gcgattcgac ccggcgagac acagcgctgg 660
 cggatcgcca acgtcagctc tgacaacttc ttctgtctgg cgctagctgg tcacacgttg 720
 caccagatcg ccgcgacgg caaccctgat gacgaggtcg ttccgcgcga ccagatcctc 780
 ctcccacctt cggagcgggt cgaggtcttg gtgcaggcat cgacccaact gggaagctac 840
 gagttccgca cctcctctg gggcgacgat ttccaggccg aaccgcagct ggtgctggcg 900
 acgatggtcg tcgctggcga ggcaatcact ccagcaccgc tccaaccgc gctcatcccc 960
 tacgaggact tgcgggatgt cccggtcgac aacatccgcg tgaccacctt cgaggaaccg 1020

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ggcgctcccc tctacctggc gatcgacggc aagcacttcg accccgaccg cgtcgaccag 1080
acgggtgaagt tggggggcgac ggaggagtgg atcgtccgca ataccagctc cgaatggcac 1140
ccgttccaca tccacgtcaa cgacttccag gtgatcgccg tcaacaacga agcgggtcaac 1200
acccatggct acgaggactc cgtcgccctc ccaccacaca gcgaaacgac gatgcggatg 1260
aaattcctcg acttcagcgg caaattcgtc taccactgcc acatcctcgg gcacgaagac 1320
ttcggcatga tggcggtagt ggaggtggtt gagtag 1356

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<210> 22

<211> 451

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<400> 22

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Met Asn Ser Leu Asp Gln Pro Gly Asp Arg Gly Glu Val Glu Gln Gln
1          5          10          15
Arg Arg Gly Pro Val Gly Gln Cys Leu Cys Pro Gly Pro Gly Gly Leu
20          25          30
Ser Leu Leu Asp Lys Ala Thr Asn Ser Gly Gln Arg Arg Leu Val Ala
35          40          45
Asp Gly Val Asp Pro Tyr Pro Gln Cys Arg Val Val Ala Thr Val Pro
50          55          60
Ala Thr Thr Arg Phe Pro Ala Ala Leu Gly Thr Gly Arg Asp Ser Pro
65          70          75          80
Val Ile Ser Gly Leu Ala Asp Val Thr Asn Leu His Thr His Gly Phe
85          90          95
His Val Ser Pro Gln Gly Asn Ser Asp Asn Ile Phe Leu His Ile Asn
100         105         110
Pro Gly Glu Thr Phe Asp Tyr Glu Phe Lys Leu Pro Ala Asn His Ser
115         120         125
Pro Gly Met Tyr Trp Tyr His Pro His Gly His Gly Asp Thr Ala Pro
130         135         140
Gln Cys Asn Gly Gly Met Ala Gly Val Ile Leu Ile Asp Gly Gly Leu
145         150         155         160
Asp Glu Val Pro Gly Ile Ala Gly Leu Thr Glu Arg Leu Leu Val Leu
165         170         175
Gln Ala Thr Gln Phe Asp Gly Asp Gly Asn Leu Val Pro Tyr Asn Asn
180         185         190
Gln Ser Asn Ala Thr Arg Gln Arg Phe Val Asn Gly Gln Leu Asn Pro
195         200         205
Thr Ile Ala Ile Arg Pro Gly Glu Thr Gln Arg Trp Arg Ile Ala Asn
210         215         220
Val Ser Ser Asp Asn Phe Leu Leu Ala Leu Ala Gly His Thr Leu
225         230         235         240
His Gln Ile Ala Ala Asp Gly Asn Pro Tyr Asp Glu Val Val Pro Arg
245         250         255
Asp Gln Ile Leu Leu Pro Pro Ser Glu Arg Val Glu Val Leu Val Gln
260         265         270
Ala Ser Thr Gln Leu Gly Ser Tyr Glu Phe Arg Thr Leu Leu Trp Gly
275         280         285
Asp Asp Phe Gln Ala Glu Pro Asp Val Val Leu Ala Thr Met Val Val
290         295         300
Ala Gly Glu Ala Ile Thr Pro Ala Pro Leu Pro Thr Ala Leu Ile Pro
305         310         315         320
Tyr Glu Asp Leu Arg Asp Val Pro Val Asp Asn Ile Arg Val Thr Thr
325         330         335
Phe Glu Glu Pro Gly Ala Pro Leu Tyr Leu Ala Ile Asp Gly Lys His

```

<210>	24
<211>	589
<212>	PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<221> SIGNAL

<222> (1)...(20)

<221> DOMAIN

<222> (197)...(352)

<223> Multicopper oxidase

<221> DOMAIN

<222> (390)...(556)

<223> Multicopper oxidase

<221> DOMAIN

<222> (59)...(194)

<223> Multicopper oxidase

<400> 24

Met	Lys	Ser	Phe	Ile	Gly	Thr	Val	Gly	Gly	Ile	Ala	Leu	Thr	Ala	Lys
1				5					10					15	
Ala	Val	Ser	Ala	Thr	Pro	Met	Leu	Phe	Asn	Glu	Pro	Ser	Thr	Asn	Val
			20					25					30		
Ala	Lys	Arg	Ala	Ala	Thr	Ser	Cys	Asn	Thr	Ala	Ser	Asn	Arg	Ser	Cys
		35					40					45			
Trp	Thr	Thr	Asp	Gly	Tyr	Thr	Ile	Asp	Thr	Asn	Tyr	Val	Val	Asp	Tyr
	50					55					60				
Pro	Thr	Thr	Gly	Val	Thr	Arg	Gln	Tyr	Thr	Leu	Tyr	Val	Thr	Glu	Val
65					70					75					80
Glu	Asn	Ala	Asn	Leu	Asp	Gly	Thr	Val	Lys	Asn	Ile	Ser	Met	Leu	Ile
				85					90					95	
Asn	Gly	Thr	Tyr	Pro	Gly	Pro	Thr	Leu	Tyr	Ala	Asp	Trp	Gly	Asp	Asp
			100					105					110		
Ile	Glu	Ile	Thr	Val	Ile	Asn	Asn	Leu	Thr	Thr	Asn	Gly	Thr	Ser	Met
		115					120					125			
His	Trp	His	Gly	Val	Thr	Gln	Leu	Asn	Thr	Asn	Ile	Met	Asp	Gly	Val
	130					135					140				
Asn	Gly	Val	Thr	Glu	Cys	Pro	Thr	Thr	Pro	Gly	Asp	Ser	His	Thr	Tyr
145					150					155					160
Lys	Phe	His	Val	Thr	Gln	Tyr	Gly	Ser	Thr	Trp	Tyr	His	Ser	His	Tyr
			165						170					175	
Ser	Thr	Gln	Tyr	Gly	Asn	Gly	Ala	Trp	Gly	Thr	Met	Ile	Phe	Asn	Gly
		180						185					190		
Pro	Ala	Ser	Ala	Asn	Tyr	Asp	Ile	Asp	Leu	Gly	Thr	Tyr	Pro	Ile	Ser
		195				200						205			
Asp	Tyr	Ile	Tyr	Ala	Thr	Ala	Glu	Ala	Val	Tyr	Ala	Glu	Tyr	Val	Ile
	210					215					220				
Pro	Ser	Pro	Gly	Val	Ala	Pro	Ser	Pro	Asn	Asn	Ile	Leu	Phe	Asn	Gly
225					230					235					240
Ser	His	Val	Asn	Val	Asp	Gly	Glu	Gly	Ser	Tyr	Asn	Val	Val	Thr	Leu
			245						250					255	
Thr	Lys	Gly	Lys	Thr	His	Arg	Leu	Arg	Leu	Ile	Asn	Thr	Ala	Ile	Asp
			260					265					270		
Ala	Glu	Met	Ile	Leu	Lys	Leu	Asn	Lys	His	Asn	Met	Thr	Val	Ile	Gln
		275				280					285				
Thr	Asp	Phe	Val	Pro	Val	Thr	Pro	Tyr	Glu	Thr	Asp	Tyr	Leu	Phe	Leu
	290					295					300				

Gly Ile Gly Gln Arg Ala Asp Val Leu Ile Thr Ala Asp Gln Asp Val
 305 310 315 320
 Asp Ser Tyr Trp Phe Asn Leu Thr Trp Pro Ser Asn Gly Leu Cys Gly
 325 330 335
 Ser Ser Lys Val Ser Tyr Pro Ala Ser Ile Phe Arg Tyr Glu Gly Ala
 340 345 350
 Thr Asp Glu Asn Pro Thr Asp Glu Gly Thr Ala Pro Ser Ser Leu Ala
 355 360 365
 Cys Asp Asp Lys Tyr Asp Tyr Glu Pro Val Val Thr Leu Ala Val Pro
 370 375 380
 Ser Glu Ser Phe Ala Glu Ser Ile Asp Ser Thr Leu Asp Val Ser Leu
 385 390 395 400
 Thr Thr Lys Thr Trp Glu Asn Ile Asp Ser Arg Val Tyr Trp Thr Val
 405 410 415
 Ser Glu Ser Ser Ile Asn Val Thr Trp Gly His Pro Thr Leu Gln Tyr
 420 425 430
 Ile Asn Glu Asn Asp Thr Ser Tyr Pro Thr Asp Leu Asn Val Leu Lys
 435 440 445
 Val Pro Asp Asn Gln Thr Trp Ala Tyr Trp Val Ile Asn Asn Glu Leu
 450 455 460
 Ser Val Pro His Pro Leu His Leu His Gly His Asp Phe Phe Val Leu
 465 470 475 480
 Gly Ser Ser Gly Thr Leu Asp Thr Ala Ala Asn Phe Asn Ala Ser Ser
 485 490 495
 Asp Leu Ser Ser Leu Asn Phe Lys Asn Pro Met Arg Arg Asp Val Thr
 500 505 510
 Met Leu Pro Gly Asn Gly Trp Val Val Met Ala Phe Glu Asn Asn Asn
 515 520 525
 Pro Gly Ala Trp Val Met His Cys His Ile Ala Trp His Val Ala Ser
 530 535 540
 Gly Leu Ser Val Gln Phe Val Glu Lys Val Asp Asp Ile Lys Ser Leu
 545 550 555 560
 Phe Asp Leu Ser Ser Val Leu Asp Asp Arg Cys Ser Ala Trp Asn Thr
 565 570 575
 Tyr Glu Ala Glu Thr Ile Tyr Lys Gln Asp Asp Ser Gly
 580 585

<210> 25

<211> 1179

<212> DNA

<213> OUnknown

<220>

<223> Obtained from an environmental sample

<400> 25

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ccagtgatca	gcgggctcgc	cgatgtcacc	aatctccaca	ctcacggctt	tcattgtttca	120
ccgcaaggga	actccgacaa	catcttcctc	cacatcaacc	ccggcgagac	cttcgactac	180
gagttcaagc	tgcccgcgaa	ccactcaccg	gggatgtact	ggtatcacc	gcattggtcac	240
ggcgacaccg	ccccccagtg	caacggcggc	atggccgggg	tgatcctgat	cgacggcggt	300
ctcgacgagg	tgccgggaat	cgccggtctg	accgaacgcc	tgctcgtcct	ccaggcgacg	360
caattcgacg	gcgacggcaa	cctcgtccct	tacaacaacc	agtcgaacgc	gactcggcag	420
cgcttcgtca	acggtcaact	caacccaacg	atcgcgattc	gaccggcgga	gacacagcgc	480
tggcggtatc	ccaacgtcag	ctctgacaac	ttcttcctgc	tggcgctagc	tggtcacacg	540
ctgcaccaga	tcgccgcgga	cggcaaccgc	tatgacgagg	tcgttcgcgc	cgaccagatc	600
ctcctccac	cctcggagcg	ggtcggagtc	ttggtgcagg	catcgaccca	actgggaagc	660
tacgagttcc	gcaccctcct	ctggggcgac	gatttcagg	ccgaaccgga	cgtggtgctg	720
gcgacgatgg	tcgtcgtctg	cgaggcaatc	actccagcac	cgctcccaac	cgcgctcatc	780


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ccctacgagg acttgcgga tgtcccggc gacaacatcc gcgtgaccac cttcgaggaa      840
ccgggcgctc ccctctacct ggcgatcgac ggcaagcact tcgaccccga ccgcgtcgac      900
cagacgggtga agttgggggc gacggaggag tggatcgctc gcaataccag ctccgaatgg      960
caccggttcc acatccacgt caacgacttc caggtgatcg ccgtcaacaa cgaagcggtc     1020
aacacccatg gctacgagga ctccgtcgcc ctcccaccac acagcgaaac gacgatgcgg     1080
atgaaattcc tcgacttcag cggcaaattc gtctaccact gccacatcct cgggcacgaa     1140
gacttcggca tgatggcggg agtggagggt gttgagtag      1179

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<210> 26

<211> 392

<212> PRT

<213> Unknown

<220>

<223> Obtained from an environmental sample

<221> DOMAIN

<222> (108)...(249)

<223> Multicopper oxidase

<400> 26

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Met Ala Thr Val Pro Ala Thr Thr Arg Phe Pro Ala Ala Leu Gly Thr
 1          5          10          15
Gly Arg Asp Ser Pro Val Ile Ser Gly Leu Ala Asp Val Thr Asn Leu
 20          25          30
His Thr His Gly Phe His Val Ser Pro Gln Gly Asn Ser Asp Asn Ile
 35          40          45
Phe Leu His Ile Asn Pro Gly Glu Thr Phe Asp Tyr Glu Phe Lys Leu
 50          55          60
Pro Ala Asn His Ser Pro Gly Met Tyr Trp Tyr His Pro His Gly His
 65          70          75          80
Gly Asp Thr Ala Pro Gln Cys Asn Gly Gly Met Ala Gly Val Ile Leu
 85          90          95
Ile Asp Gly Gly Leu Asp Glu Val Pro Gly Ile Ala Gly Leu Thr Glu
100          105          110
Arg Leu Leu Val Leu Gln Ala Thr Gln Phe Asp Gly Asp Gly Asn Leu
115          120          125
Val Pro Tyr Asn Asn Gln Ser Asn Ala Thr Arg Gln Arg Phe Val Asn
130          135          140
Gly Gln Leu Asn Pro Thr Ile Ala Ile Arg Pro Gly Glu Thr Gln Arg
145          150          155          160
Trp Arg Ile Ala Asn Val Ser Ser Asp Asn Phe Phe Leu Leu Ala Leu
165          170          175
Ala Gly His Thr Leu His Gln Ile Ala Ala Asp Gly Asn Pro Tyr Asp
180          185          190
Glu Val Val Pro Arg Asp Gln Ile Leu Leu Pro Pro Ser Glu Arg Val
195          200          205
Glu Val Leu Val Gln Ala Ser Thr Gln Leu Gly Ser Tyr Glu Phe Arg
210          215          220
Thr Leu Leu Trp Gly Asp Asp Phe Gln Ala Glu Pro Asp Val Val Leu
225          230          235          240
Ala Thr Met Val Val Ala Gly Glu Ala Ile Thr Pro Ala Pro Leu Pro
245          250          255
Thr Ala Leu Ile Pro Tyr Glu Asp Leu Arg Asp Val Pro Val Asp Asn
260          265          270
Ile Arg Val Thr Thr Phe Glu Glu Pro Gly Ala Pro Leu Tyr Leu Ala
275          280          285
Ile Asp Gly Lys His Phe Asp Pro Asp Arg Val Asp Gln Thr Val Lys
290          295          300

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Leu	Gly	Ala	Thr	Glu	Glu	Trp	Ile	Val	Arg	Asn	Thr	Ser	Ser	Glu	Trp
305					310					315					320
His	Pro	Phe	His	Ile	His	Val	Asn	Asp	Phe	Gln	Val	Ile	Ala	Val	Asn
			325						330						335
Asn	Glu	Ala	Val	Asn	Thr	His	Gly	Tyr	Glu	Asp	Ser	Val	Ala	Leu	Pro
			340						345					350	
Pro	His	Ser	Glu	Thr	Thr	Met	Arg	Met	Lys	Phe	Leu	Asp	Phe	Ser	Gly
		355					360					365			
Lys	Phe	Val	Tyr	His	Cys	His	Ile	Leu	Gly	His	Glu	Asp	Phe	Gly	Met
	370					375					380				
Met	Ala	Val	Val	Glu	Val	Val	Glu								
385					390										